

#5
Pfarrer
1.22.01RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/598,042A
DATE: 01/16/2001
TIME: 17:34:43Input Set : D:\PT_FL.784CIP2.061400
Output Set: N:\CRF3\01162001\I598042A.rawENTERED
see p. 5

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6 <110> APPLICANT: Tang, Y. Tom
7   Liu, Chenghua
8   Asundi, Vinod
9   Xu, Chongjun
10  Zhou, Ping
11  Ma, Yunqing
12  Wang, Jian-Rui
13  Zhao, Qing A.
14  Ren, Feiyan
15  Chen, Rui-hong
16  Wang, Dunrui
17  Wang, Zhiwei
18  Wehrman, Tom
19  Zhang, Jie
20  Qian, Xiaohong B.
21  Drmanac, Radoje T.
24 <120> TITLE OF INVENTION: Novel Nucleic Acids and
25   Polypeptides
29 <130> FILE REFERENCE: 784CIP2
31 <140> CURRENT APPLICATION NUMBER: US/09/598,042A
32 <141> CURRENT FILING DATE: 2000-06-20
35 <150> PRIOR APPLICATION NUMBER: 09/552,317
36 <151> PRIOR FILING DATE: 2000-04-25
38 <150> PRIOR APPLICATION NUMBER: 09/488,725
39 <151> PRIOR FILING DATE: 2000-01-21
41 <160> NUMBER OF SEQ ID NOS: 331
43 <170> SOFTWARE: pt_FL_genes Version 1.0
49 <210> SEQ ID NO: 1
50 <211> LENGTH: 1630
51 <212> TYPE: DNA
52 <213> ORGANISM: Homo sapiens
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55 <221> NAME/KEY: CDS
56 <222> LOCATION: (261)..(1052)
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63   aggcccttca ttagacacta atttgaagct atggcattcc cccactatga gcccacctgt      180
65   cagccaggct atctgccttg atcctagatg aagtggccat tctgcttgcc cctcagaacc      240
67   tctctgtact ctcaaccaac  \atg aag cat ctc ttg atg tgg agc cca gtc      290
68                               Met Lys His Leu Leu Met Trp Ser Pro Val
69                               1           5           10
71   atc gcg cct gga gaa aca gtc tac tat tct gtc gaa tac cag ggg gag      338
72   Ile Ala Pro Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu
73                               15           20           25
75   tac gag agc ctg tac acg agc cac atc tgg atc ccc agc agc tgg tgc      386
76   Tyr Glu Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys

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77          30          35          40
79 tca ctc act gaa ggt cct gag tgt gat gtc act gat gac atc acg gcc 434
80 Ser Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala
81          45          50          55
83 act gtg cca tac aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc 482
84 Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr
85          60          65          70
87 tca gcc tgg agc atc ctg aag cat ccc ttt aat aga aac tca acc atc 530
88 Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile
89          75          80          85          90
91 ctt acc cga cct ggg atg gag atc acc aaa gat ggc ttc cac ctg gtt 578
92 Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val
93          95          100          105
95 att gag ctg gag gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac 626
96 Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr
97          110          115          120
99 tgg agg agg gag cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt 674
100 Trp Arg Arg Gln Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser
101          125          130          135
103 ggg ggt att cca ttg cac cta gaa acc atg gag cca ggg gct gca tac 722
104 Gly Gly Ile Pro Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr
105          140          145          150
107 tgt gtg aag gcc cag aca ttc gtg aag gcc att ggg agg tac agc gcc 770
108 Cys Val Lys Ala Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala
109          155          160          165          170
111 ttc agc cag aca gaa tgt gtg gag gtg caa gga gag gcc att ccc ctg 818
112 Phe Ser Gln Thr Glu Cys Val Glu Val Gln Gly Glu Ala Ile Pro Leu
113          175          180          185
115 gta ctg gcc ctg ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc 866
116 Val Leu Ala Leu Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val
117          190          195          200
119 gtg cca ctg ttc gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt 914
120 Val Pro Leu Phe Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys
121          205          210          215
123 tgc ccc gtg gtg gtc ctc cca gac acc ttg aaa ata acc aat tca ccc 962
124 Cys Pro Val Val Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro
125          220          225          230
127 cag aag tta atc agc tgc aga agg gag gag gtg gat gcc tgt gcc acg 1010
128 Gln Lys Leu Ile Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr
129          235          240          245          250
131 gct gtg atg tct cct gag gaa ctc ctc agg gcc tgg atc tca taggttt 1059
132 Ala Val Met Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
133          255          260
135 gcggaagggc ccagggtgaag ccgagaacct ggtctgcatg acatggaac catgagggga 1119
137 caagtttgtt ttctgttttc cggcaccggac aagggtatgag agaagtagga agagcctgtt 1179
139 gtctacaagt ttagaagcaa ccatcagagg cagggtggtt tgtctaacag aacctgact 1239
141 gaggttagg ggaatgtgacc tctagactgg gggtgccac ttgctgctg agcaacctg 1299
143 ggaanaagtga cttcatccct ccgtccctaa gttttctcat ctglaatggg ggaattacct 1359
145 acacacctgc taacacacaa cacacagagt ctctctctat atatacacac gtacacataa 1419

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147 atacaccag cacttgcaag qctagagggg aactgggtgac actctacagt ctgactgatt 1479
149 cagtgttict ggagagcagg acataaatgt atgatgagaa tgatcaagga ctctacacac 1539
151 tgggtggctt ggaaagccca ctttcccaga ataatccttg agagaaaaag aatcatggga 1599
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161 <213> ORGANISM: Homo sapiens
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165 <222> LOCATION: (22)..(1848)
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169 Met Leu Pro Ala Ala Met Ala Ala Gly Leu
170 1 5 10
172 tcc ttc atc cac qtg atg tgg ttc ccg ggt cga cga ttt cgt cgg cag 99
173 Ser Phe Ile His Val Met Ser Phe Pro Gly Arg Arg Phe Arg Arg Gln
174 15 20 25
176 qtg gcc cgg ctg qgc cgc act atg ccg ctg cag tgc cca qtg gag qgg 147
177 Val Ala Arg Leu Gly Arg Thr Met Arg Leu Gln Cys Pro Val Glu Gly
178 30 35 40
180 gac ccg ccg ccg ctg acc atg tgg acc aag gat ggc cgc acc atc cac 195
181 Asp Pro Pro Pro Leu Thr Met Trp Thr Lys Asp Gly Arg Thr Ile His
182 45 50 55
184 agc ggc tgg agc cgc ttc cgc gtg ctg ccg cag ggg ctg aag gtg aag 243
185 Ser Gly Trp Ser Arg Phe Arg Val Leu Pro Gln Gly Leu Lys Val Lys
186 60 65 70
188 cag gtg gag cgg gag gat gcc ggc gtg tac gtg tgc aag gcc acc aac 291
189 Gln Val Glu Arg Glu Asp Ala Gly Val Tyr Val Cys Lys Ala Thr Asn
190 75 80 85 90
192 ggc ttc ggc agc ctg agc gtc aac tac acc ctc gtc gtg ctg gat gac 339
193 Gly Phe Gly Ser Leu Ser Val Asn Tyr Thr Leu Val Val Leu Asp Asp
194 95 100 105
196 att agc cca ggg aag gag agc ctg ggg ccc gac agc tcc tct ggg ggt 387
197 Ile Ser Pro Gly Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly
198 110 115 120
200 caa gag gac ccc gcc agc cag cag tgg gca cga ccg cgc ttc aca cag 435
201 Gln Glu Asp Pro Ala Ser Glu Gln Trp Ala Arg Pro Arg Phe Thr Gln
202 125 130 135
204 ccc tcc aag atg agg cgc ccg gtg atc gca cgg ccc gtg ggt agc tcc 483
205 Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly Ser Ser
206 140 145 150
208 gtg ccg ctc aag tgc gtg gcc agc ggg cac cct cgg ccc gac atc acg 531
209 Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro Asp Ile Thr
210 155 160 165 170
212 tgg atg aag gac gac cag gcc ttg acg cgc cca gag gcc gct gag ccc 579
213 Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu Ala Ala Glu Pro
214 175 180 185
216 agg aag aag aag tgg aca ctg agc ctg aag aac ctg cgg ccg gag gac 627

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217 Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn Leu Arg Pro Glu Asp
218          190          195          200
220 agc qgc aaa tac acc tgc cgc gtg tgc aac cgc qgc gcc atc aac 675
221 Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn Arg Ala Gly Ala Ile Asn
222          205          210          215
224 gcc acc tac aag gtg gat gtg atc cag cgg acc cgt tcc aag ccc gtg 723
225 Ala Thr Tyr Lys Val Asp Val Ile Gln Arg Thr Arg Ser Lys Pro Val
226          220          225          230
228 ctc aca ggc acg cac ccc gtg aac acg acg gtg gac ttc ggg ggg acc 771
229 Leu Thr Gly Thr His Pro Val Asn Thr Thr Val Asp Phe Gly Gly Thr
230          235          240          245          250
232 acg tcc ttc cag tgc aag gtg cgc agc gac gtg aag cgg gtg atc cag 819
233 Thr Ser Phe Gln Cys Lys Val Arg Ser Asp Val Lys Pro Val Ile Gln
234          255          260          265
236 tgg ctg aag cgc gtg gag tac ggc gcc gag ggc cgc cac aac tcc acc 867
237 Trp Leu Lys Arg Val Glu Tyr Gly Ala Glu Gly Arg His Asn Ser Thr
238          270          275          280
240 atc gat gtg ggc ggc cag aag ttt gtg gtg ctg ccc acg ggt gac gtg 915
241 Ile Asp Val Gly Gly Gln Lys Phe Val Val Leu Pro Thr Gly Asp Val
242          285          290          295
244 tgg tgc cgg ccc gac ggc tcc tac ctc aat aag ctg ctc atc acc cgt 963
245 Trp Ser Arg Pro Asp Gly Ser Tyr Leu Asn Lys Leu Leu Ile Thr Arg
246          300          305          310
248 gcc cgc cag gac gat ggc ggc atg tac atc tgc ctt ggc gcc aac acc 1011
249 Ala Arg Gln Asp Asp Ala Gly Met Tyr Ile Cys Leu Gly Ala Asn Thr
250          315          320          325          330
252 atg qgc tac agc ttc cgc agc gcc ttc ctc acc gtg ctg cca gac cca 1059
253 Met Gly Tyr Ser Phe Arg Ser Ala Phe Leu Thr Val Leu Pro Asp Pro
254          335          340          345
256 aaa cgg cca ggg cca cct gtg gcc tcc tgc tcc tgc gcc act agc ctg 1107
257 Lys Pro Pro Gly Pro Pro Val Ala Ser Ser Ser Ala Thr Ser Leu
258          350          355          360
260 cgg tgg ccc gtg gtc atc ggc atc cca gcc ggc gct gtc ttc atc ctg 1155
261 Pro Trp Pro Val Val Ile Gly Ile Pro Ala Gly Ala Val Phe Ile Leu
262          365          370          375
264 ggc acc ctg ctc ctg tgg ctt tgc cag gcc cag aag aag cgg tgc acc 1203
265 Gly Thr Leu Leu Leu Trp Leu Cys Gln Ala Gln Lys Lys Pro Cys Thr
266          380          385          390
268 ccc gcg cct gcc cct ccc ctg cct ggg cac cgc cgg cgg ggg acg gcc 1251
269 Pro Ala Pro Ala Pro Pro Leu Pro Gly His Arg Pro Pro Gly Thr Ala
270          395          400          405          410
272 cgc gac cgc agc gga gac aag gac ctt ccc tgc ttg gcc gcc ctc agc 1299
273 Arg Asp Arg Ser Gly Asp Lys Asp Leu Pro Ser Leu Ala Ala Leu Ser
274          415          420          425
276 gct ggc cct ggt gtg ggg ctg tgt gag gag cat ggg tct cgg gca gcc 1347
277 Ala Gly Pro Gly Val Gly Leu Cys Glu Glu His Gly Ser Pro Ala Ala
278          430          435          440
280 ccc cag cac tta ctg ggc cca ggc cca gtt gct ggc cct aag ttg tac 1395
281 Pro Gln His Leu Leu Gly Pro Gly Pro Val Ala Gly Pro Lys Leu Tyr

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282          445          450          455
284 ccc aaa ctc tac aca gac atc cac aca cac aca cac tgt att gcg gcc 1443
285 Pro Lys Leu Tyr Thr Asp Ile His Thr His Thr His Cys Ile Ala Ala
286          460          465          470
288 gcc tgt gtg agg agc atg qgt ctc cgg cag ccc ccc agc act tac tgg 1491
289 Ala Cys Val Arg Ser Met Gly Leu Arg Gln Pro Pro Ser Thr Tyr Trp
290 475          480          485          490
292 gcc cag gcc cag ttg ctg gcc cta agt tgt acc cca aac tct aca cag 1539
293 Ala Gln Ala Gln Leu Leu Ala Leu Ser Cys Thr Pro Asn Ser Thr Gln
294          495          500          505
296 aca tcc aca cac aca cac aca act ctc aca cac act cac acg tgg 1587
297 Thr Ser Thr His Thr His Thr His Thr Leu Thr His Thr His Thr Trp
298          510          515          520
300 agg gca agg tcc acc agc aca tcc act atc agt gct aga cgg cac cgt 1635
301 Arg Ala Arg Ser Thr Ser Thr Thr Ile Ser Ala Arg Arg His Arg
302          525          530          535
304 atc tgc aga ggg cac ggg ggg gcc qgc cag aca ggc aga ctg gga gga 1683
305 Ile Cys Arg Gly His Gly Gly Ala Gly Gln Thr Gly Arg Leu Gly Gly
306          540          545          550
308 tgg agg acg gag ctg cag acg aag gca ggg gac cca tgg cga gga gga 1731
309 Trp Arg Thr Gln Leu Gln Thr Lys Ala Gly Asp Pro Trp Arg Gly Gly
310 555          560          565          570
312 atg gcc agc acc cca ggc agt ctg tgt gtg agg cat agc ccc tgg aca 1779
313 Met Ala Ser Thr Pro Gly Ser Leu Cys Val Arg His Ser Pro Trp Thr
314          575          580          585
316 cac aca cac aga cac aca cac tac ctg gat gca tgt atg cac aca cat 1827
317 His Thr His Arg His Thr His Tyr Leu Asp Ala Cys Met His Thr His
318          590          595          600
320 gcg cgc aca cgt gct ccc tga ag gcacacgtac gcacacacgc acatgcacag 1880
W--> 321 Ala Arg Thr Arg Ala Pro *
322          605
324 atatgccgcc tggggcacaca gataagctgc ccaaatgcac gcacacgcac agagacatgc 1940
326 cagaacatac aaggacatgc tgcctgaaca tacacacgca caccatgcg cagatgtgct 2000
328 gacctggacac acacacacac acggatatgc tgtctggacg cacacacgtg cagatatggt 2060
330 atccggacac acacgtgcac agatatgctg cctggacaca cagataatgc tgccttgaca 2120
332 cacacatgca cggatatattgc ctggacacac acacacacac gtgtgcacag atatgctgtc 2180
334 tggacacgca cacacatgca gatattgctg ctggacacac acttcacagc acacgtgcac 2240
336 aggcgcagat atgctgctg gcacacacgc gatattgctg ctagtccac acacacgcag 2300
338 acatgctgtc cggacacaca cacqcatgca cagatatgct gtccggacac acacacgcac 2360
340 gcagatatgc tgcctggaca cacacacaga taatgctgcc tcaacactca cacacgtgca 2420
342 gatattgctt ggcacacac atgtgcacag atatgctgtc tggacatgca cacacgtgca 2480
344 gatattgctt cgggatacac acgcacgcac acatgcagat atgctgctg ggcacacact 2540
346 tcgggacaca catgcacaca caggtgcaga tatgctgctt ggacacacgc agactgacgt 2600
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354 ctgggtgcc caggagtccc ctactgctgt gggtgggtt tgggggcaca gcagccccaa 2840
356 gcttgagag ctggagccca tggctagtgg ctcatcccca ctgcattctc cccctgcac 2900
358 agagaagggg ccttggattt tatatttaag aatgaagat aatattaata atgatggaag 2960

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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Input Set : D:\PT_FL.784CIP2.061400

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L:321 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 2
L:530 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 3
L:4083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:5705 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 17
L:5764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:6187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:6784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:7352 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 25
L:8768 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 36
L:11219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:11605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:11607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:11683 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 49
L:14743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:14997 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 62
L:15505 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:65
L:15910 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67
L:15991 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 67
L:16993 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 71
L:17617 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:76
L:18052 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 78
L:19453 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:86
L:20052 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 90
L:20340 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 92
L:21215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95
L:21268 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 95
L:22125 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 100
L:22403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:101
L:22868 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103
L:23440 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 106
L:25322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116
L:25547 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 118
L:26164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123
L:26168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123
L:26405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:125
L:26407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:125
L:26788 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:128
L:26908 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:129
L:27068 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:131
L:27342 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 134
L:27522 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:135
L:29018 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 142
L:29766 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 147
L:31572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:158
L:31574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:158
L:31711 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:160
L:31713 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:160
L:32072 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 164

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Input Set : D:\PT_FL.784CIP2.061400

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L:32163 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 165
L:32306 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 166
L:32542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:167
L:32716 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:169
L:32964 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 170
L:33067 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 171
L:33317 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 173
L:33645 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 175
L:34362 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:181
L:34454 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 182
L:34863 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 185
L:35201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:187
L:35203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:187
L:35362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:189
L:35448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:190
L:35576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:190
L:35580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:190
L:35582 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:190
L:35588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:190
L:35618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:35740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:35744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:35746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:35752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:37011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:199
L:37370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:201
L:37512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:38004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:205
L:38537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:209
L:38947 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 212
L:39437 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:215
L:39648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:40703 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:224
L:42404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:234
L:42406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:234
L:43386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:243
L:43602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:244
L:44238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:249
L:46041 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:262
L:46043 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:262
L:46505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:267
L:46620 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:268
L:46844 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:270
L:47265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:273
L:47593 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:275
L:47720 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:276
L:47798 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 277
L:47917 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 278
L:47988 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 279

VERIFICATION SUMMARY

DATE: 01/16/2001

PATENT APPLICATION: US/09/598,042A

TIME: 17:34:44

Input Set : D:\PT_FL.784CIP2.061400

Output Set: N:\CRF3\01162001\I598042A.raw

L:48219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:282
L:48722 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 284
L:48871 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 285
L:49043 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 287
L:49358 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 290
L:49456 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:291
L:49480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:292
L:50060 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 295
L:50364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:296
L:50914 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 299
L:51701 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 304
L:52169 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 306
L:52633 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 310
L:52664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:311
L:53674 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:315
L:53790 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 316
L:53920 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 317
L:54652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:323
L:55205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:326